IN THE CLAIMS

The status of each claim is listed below.

1. (Currently Amended) A transformed microorganism belonging to enterobacteria and having L-glutamic acid productivity, into which a citrate synthase gene obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum* ~~a coryneform bacterium~~ is introduced.

2. (Currently Amended) The microorganism of claim 1 wherein a citrate synthase gene from ~~the coryneform bacterium is~~ *Brevibacterium lactofermentum* is introduced.

Claims 3-5: Canceled.

6. (Previously Presented) The microorganism of claim 1 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

7. (Previously Presented) The microorganism of claim 2 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

8. (Previously Presented) The microorganism of claim 6 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

9. (Previously Presented) The microorganism of claim 7 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

10. (Previously Presented) A process for producing L-glutamic acid comprising the steps of culturing the microorganism of claim 1 in a liquid medium to produce and accumulate L-glutamic acid in the medium and collecting the L-glutamic acid from the medium.

11. (Currently Amended) A process for producing L-glutamic acid comprising

isolating a coryneform bacterium citrate synthase gene, wherein the citrate synthase gene is obtainable by PCR amplification of chromosomal DNA using primers of SEQ ID NO: 1 and SEQ ID NO: 2 ~~by amplifying the gene with oligonucleotide primers comprising SEQ ID NOS: 1 and 2~~;

transforming a enterobacteria with said isolated citrate synthase gene;

culturing said enterobacteria in a liquid medium to produce and accumulate the L-glutamic acid; and

collecting the L-glutamic acid produced.

12. (Currently Amended) The process of Claim 11, wherein the coryneform bacteria is *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*.

13. (Previously Presented) The process of Claim 11, wherein the entereobacteria is of the genus *Enterobacter* or *Klebsiella*.

14. (Previously Presented) The process of Claim 11, wherein the enterobacteria is *Enterobacter agglomerans* or *Klebsiella planticola*.

Claim 15: Cancelled.

16. (Currently Amended) The microorganism of claim 1, wherein the citrate synthase gene is obtained from corynebacterium chromosomal DNA by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2 ~~based on the nucleotide sequence of Corynebacterium glutamicum citrate synthase gene~~.

Claims 17-27: Cancelled.

28. (New) The microorganism of Claim 1, wherein the citrate synthase gene is obtained from *Corynebacterium glutamicum*.

29. (New) The microorganism of claim 28 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

30. (New) The microorganism of claim 29 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

31. (New) The microorganism of claim 29 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

32. (New) The microorganism of claim 30 wherein the bacterium is *Enterobacter agglomerans* or *Klebsiella planticola*.

33. (New) The microorganism of claim 11 wherein the microorganism belonging to enterobacteria is a bacterium belonging to the genus *Enterobacter* or *Klebsiella*.

SUPPORT FOR THE AMENDMENTS

Claim 1 has been amended to specify a citrate synthase gene obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*. See also Claims 2 and 28. Claims 11 and 16 have been amended to specify SEQ ID NO: 1 and 2 as primers. Claim 12 has been amended to specify that the coryneform bacteria is *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*. Claims 29-33 are newly-added. These amendments are supported by the specification at pages 4-32. No new matter is believed to have been added to the present application by the amendments submitted above.